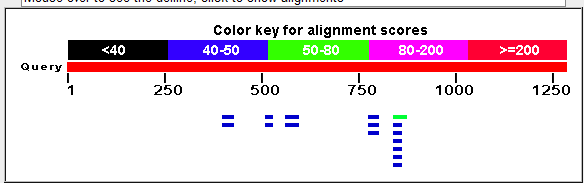
NNNNNNNNNNNTATNGNATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCTGCAGGCGGCCGCACTAGTGATTTTGATTGATTGAAGGAGAAATATCATGAGTGTGATCGCTAAACAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAGGGTGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACTGTCTCAATACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGATTATGTAAAGCAGTCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAAATCTCTGGTGTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGTGGTTACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAGGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAGTCACAACAAGGATTACACATTTGTTGAGCAGTGTGAAATATCCATTGCACGCCACTCTTTGCTCGGTCATCACCATCACCATCACTAAAATCCCGCGGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAANAGGCCCGCACCGATCGCCCTTCCCACAGTTGCGCAGCCTGATGGCNATGGACGCNNCCTGNANCGNCGCATTAGCNCGGCNGGNNNGNGNNCNCGCAGCGNGACNCTACANTTNCNGCNNCNANCNNNNNCNTTCNNTTNTNCNNNTNNNNNNNNNNNNNNNTTNCCGNNAGNTNNAANNGGGGNNNNNNNNNATNNGNTNNNNNNNNNNCCAAANTGNNNGNNNNGNNNNNNNNGNNNNNNNNNNNNNNNNNNNNNNNGANCNNNNNNNNNNNNANNNNNNNNNNNCNNNNNAANNNNNCCNNTNNN

Chopped version:

TATNGNATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCTGCAGGCGGCCGCACTAGTGATTTTGATTGATTGAAGGAGAAATATCATGAGTGTGATCGCTAAACAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAGGGTGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACTGTCTCAATACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGATTATGTAAAGCAGTCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAAATCTCTGGTGTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGTGGTTACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAGGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAGTCACAACAAGGATTACACATTTGTTGAGCAGTGTGAAATATCCATTGCACGCCACTCTTTGCTCGGTCATCACCATCACCATCACTAAAATCCCGCGGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAANAGGCCCGCACCGATCGCCCTTCCCACAGTTGCGCAGCCTGATGGCNATGGACGCNNCCTGNANCGNCGCATTAGCNCGGCNGGNNNGNGNNCNCGCAGCGNGACNCTACANTTNCNGCNNCNANC

Rule of thumb: You see five N’s that’s when you chop the DNA sequence.

Figure 1: Nucleotide Blast of VDS4\_M13R\_pGBR22 against human nucleotides



Did you find anything that is similar to your sequence? How close are they? What is it?

It’s not a good match to the human DNA nucleotides. The following sequence is not close, and it is Montipora efflorescens GFP-like chromoprotein mRNA.

Figure 2: Nucleotide Sequence (684 letters)

>lcl|15393

Length=1092

Score = 1258 bits (681), Expect = 0.0

Identities = 683/684 (99%), Gaps = 0/684 (0%)

Strand=Plus/Plus

Query 1 ATGAGTGTGATCGCTAAACAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGA 60

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 105 ATGAGTGTGATCGCTAAACAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGA 164

Query 61 CACTACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTA 120

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 165 CACTACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTA 224

Query 121 AAGCTCACTGTCACCAAGGGTGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACTG 180

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 225 AAGCTCACTGTCACCAAGGGTGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACTG 284

Query 181 TCTCAATACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGATTATGTAAAG 240

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 285 TCTCAATACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGATTATGTAAAG 344

Query 241 CAGTCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTG 300

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 345 CAGTCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTG 404

Query 301 TGTACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAAATC 360

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 405 TGTACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAAATC 464

Query 361 TCTGGTGTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAA 420

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 465 TCTGGTGTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAA 524

Query 421 CCCAACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCT 480

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 525 CCCAACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCT 584

Query 481 CTGAAGTTGGAAGGAGGTGGTTACTATTTGTGTGAGTTCAAATCTACTTACAAGGCAAAG 540

||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||

Sbjct 585 CTGAAGTTGGAAGGAGGTGGTTACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAG 644

Query 541 AAGCCTGTGAGGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAGTCAC 600

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 645 AAGCCTGTGAGGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAGTCAC 704

Query 601 AACAAGGATTACACATTTGTTGAGCAGTGTGAAATATCCATTGCACGCCACTCTTTGCTC 660

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 705 AACAAGGATTACACATTTGTTGAGCAGTGTGAAATATCCATTGCACGCCACTCTTTGCTC 764

Query 661 GGTCATCACCATCACCATCACTAA 684

||||||||||||||||||||||||

Sbjct 765 GGTCATCACCATCACCATCACTAA 788

Can you see any mismatches between the two? If so, is it a problem? Why or why not?

I see one mismatch, a guanine and an adenine pair. Yes the mismatched pair is a problem because this indicates a mutation in the DNA, and this may cause a problem with the creation of proteins.

Figure 3: Translated PGBR sequence

>rf 1 Untitled

YXILKLCIQRVGSSPIWSTCRRPH\*\*F\*LIEGEIS\*V\*SLNK\*PTRFICQARSMDTTLRS

KAMEKESLTRGSRR\*SSLSPRVDLCHLLGIFYHHCLNTEAYHSPSTLKTSLIM\*SSHSLR

DIHGRGS\*TLKMVQCVLSAMIPASKATVSSTMSKSLV\*TFLPMDLLCRRRHRAGNPTLSV

SLHEMEC\*\*ETTLWL\*SWKEVVTICVNSNLLTRQRSL\*GCQGITMLTANWM\*PVTTRITH

LLSSVKYPLHATLCSVITITITKIPRPWRPGACDVGPNSPYSESYYNSLAVVLQRRDWEN

PGVTQLNRLAAHPPFASWRNSEXARTDRPSHSCAA\*WXWTXPXXXH\*XGXXXXXQRDXTX

XAXX

>rf 2 Untitled

XXYSSYASNALGALPYGRPAGGRTSDFD\*LKEKYHECDR\*TNDLQGLYVRHGQWTLL\*GR

RRWKRKALRGGADGKAHCHQGWTSAICLGYFITTVSIRKHTIHQVP\*RHP\*LCKAVIP\*G

IYMGEDHEL\*RWCSVYCQQ\*FQHPRQLFHLQCQNLWCELSSQWTCYAEEDTGLGTQH\*AS

LCTRWNADRKQLYGSEVGRRWLLFV\*IQIYLQGKEACEDARVSLC\*PQTGCNQSQQGLHI

C\*AV\*NIHCTPLFARSSPSPSLKSRGHGGREHATSGPIRPIVSRITIHWPSFYNVVTGKT

LALPNLIALQHIPLSPAGVIAXRPAPIALPTVAQPDGXGRXLXRRISXAGXXXRSXTLXX

XXX

>rf 3 Untitled

XXTQAMHPTRWELSHMVDLQAAALVILID\*RRNIMSVIAKQMTYKVYMSGTVNGHYFEVE

GDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPLSQYGSIPFTKYPEDIPDYVKQSFPEG

YTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKISGVNFPPNGPVMQKKTQGWEPNTERL

FARDGMLIGNNFMALKLEGGGYYLCEFKSTYKAKKPVRMPGYHYVDRKLDVTSHNKDYTF

VEQCEISIARHSLLGHHHHHH\*NPAAMAAGSMRRRAQFAL\*\*VVLQFTGRRFTTS\*LGKP

WRYPT\*SPCSTSPFRQLA\*\*RXGPHRSPFPQLRSLMAMDAXXXXALARXXXXXAAXXYXX

XXX

Reading frame 3

6 H’s row: histidine

The third reading frame is the right reading frame. The start codon is indicated with the methionine group and the stop codon is indicated by the asterisk. The 6 His was found.

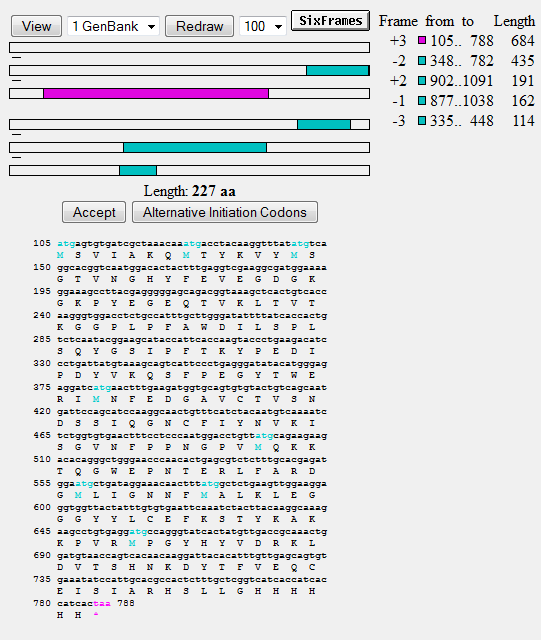
\*= indicates the stop codon

Figure 4: Reading Frame 1 for Purple Protein

>rf 1 Untitled

MSVIAKQMTYKVYMSGTVNGHYFEVEGDGKGKPYEGEQTVKLTVTKGGPLPFAWDILSPL

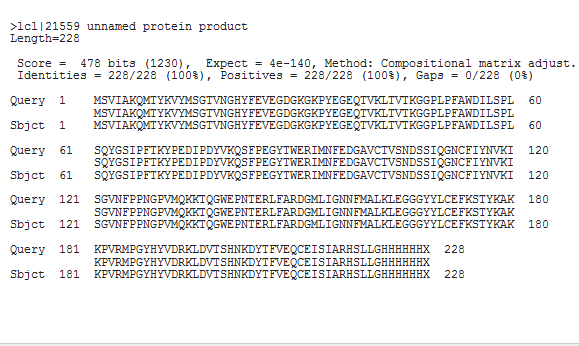
SQYGSIPFTKYPEDIPDYVKQSFPEGYTWERIMNFEDGAVCTVSNDSSIQGNCFIYNVKI

SGVNFPPNGPVMQKKTQGWEPNTERLFARDGMLIGNNFMALKLEGGGYYLCEFKSTYKAK

KPVRMPGYHYVDRKLDVTSHNKDYTFVEQCEISIARHSLLGHHHHHH\*

6 H tag = Genetically engineered affinity tag = to physically separate from another protein

Figure 5: Protein Alignment of M13PGBR22 with Purple Protein



The following protein mutation does not have an effect on the protein sequence.

Figure 6 :PGEMT sequence

GGGCGAATTGGGCCCGACGTCGCATGCTCCCGGCCGCCATGGCCGCGGGATTAATCACTAGT

GCGGCCGCCTGCAGGTCGACCATATGGGAGAGCTCCCAACGCGTTGGATGCATAGCTTGA

GTATTCTATAGTGTCACCTAAATAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGT

GAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAG

CCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTT

TCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAG

GCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCG

TTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAAT

CAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA

AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAA

ATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTC

CCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGT

CCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCA

GTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCG

ACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTAT

CGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA

CAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCT

GCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC

AAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAA

AAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAA

ACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTT

TAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACA

GTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCA

TAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCC

CCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAA

ACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCC

AGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCA

ACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCAT

TCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAG

CGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCAC

TCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTT

CTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTT

GCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGC

TCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGAT

CCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCA

GCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGA

CACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGG

GTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGG

TTCCGCGCACATTTCCCCGAAAAGTGCCACCTGATGCGGTGTGAAATACCGCACAGATGC

GTAAGGAGAAAATACCGCATCAGGAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGT

TAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTT

ATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTC

CACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATG

GCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCAC

TAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACG

TGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAG

CGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGT

CCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCT

ATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGG

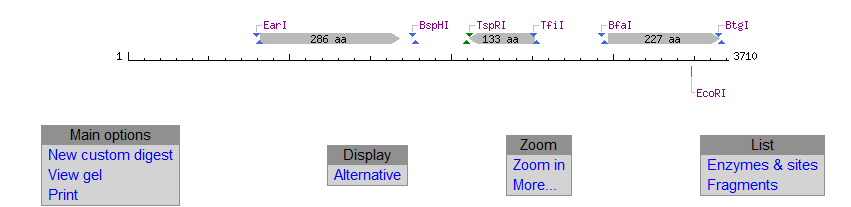
GTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGTAATACGACTCACTATA

Figure 7: Reverse Component of pgBR22

>Untitled reverse complement

TATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACA**CAGGAAACAGCTATGAC**CATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTATGCATCCAACGCGTTGGGAGCTCTCCCATATGGTCGACCTGCAGGCGGCCGCACTAGTGATTTTGATTGATTGAAGGAGAAATATCATGAGTGTGATCGCTAAACAAATGACCTACAAGGTTTATATGTCAGGCACGGTCAATGGACACTACTTTGAGGTCGAAGGCGATGGAAAAGGAAAGCCTTACGAGGGGGAGCAGACGGTAAAGCTCACTGTCACCAAGGGTGGACCTCTGCCATTTGCTTGGGATATTTTATCACCACTGTCTCAATACGGAAGCATACCATTCACCAAGTACCCTGAAGACATCCCTGATTATGTAAAGCAGTCATTCCCTGAGGGATATACATGGGAGAGGATCATGAACTTTGAAGATGGTGCAGTGTGTACTGTCAGCAATGATTCCAGCATCCAAGGCAACTGTTTCATCTACAATGTCAAAATCTCTGGTGTGAACTTTCCTCCCAATGGACCTGTTATGCAGAAGAAGACACAGGGCTGGGAACCCAACACTGAGCGTCTCTTTGCACGAGATGGAATGCTGATAGGAAACAACTTTATGGCTCTGAAGTTGGAAGGAGGTGGTTACTATTTGTGTGAATTCAAATCTACTTACAAGGCAAAGAAGCCTGTGAGGATGCCAGGGTATCACTATGTTGACCGCAAACTGGATGTAACCAGTCACAACAAGGATTACACATTTGTTGAGCAGTGTGAAATATCCATTGCACGCCACTCTTTGCTCGGTCATCACCATCACCATCACTAAAATCCCGCGGCCATGGCGGCCGGGAGCATGCGACGTCGGGCCCAATTCGCCC

Figure 8: PGBR 22 cut with ECORI



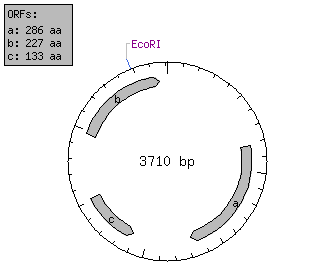
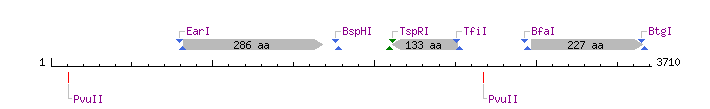


Figure 9: PGBR22 cut with PVUII



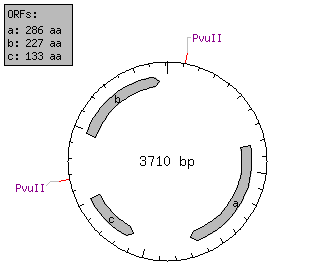
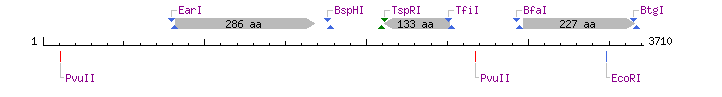
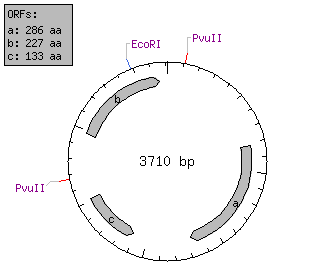


Figure 10: PGBRR22 cut with PVUII and ECORI

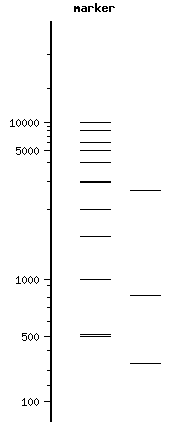


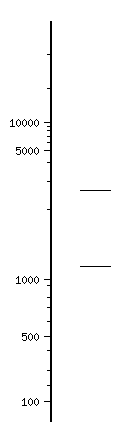


What buffers do these enzymes take? Could they be run together in the same reaction in the lab?

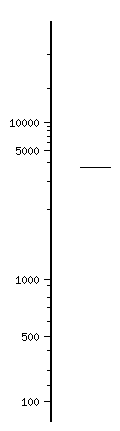
The buffers the enzymes take or the NEBuffer 2 and NEBuffer ECORI. You can use NEBuffer 2 can be used in the same reaction in the lab, works 100% for both.

Gel for PGBR22 cut with PVU2 and ECORI (both), with ECORI, PVU2





Gel for PGBR22 cut with ECORI



Question:

DNA sequencing with the forward and reverse primers that way you can combine both sequences.